

Query= SEQ ID NO:43  
(1650 letters)

Sequences producing significant alignments:	Score (bits)	E Value
AC018552.5.95189.106311	569	e-159
AC018552.5.17437.94328	297	1e-77

>AC018552.5.95189.106311  
Length = 11123

Score = 569 bits (287), Expect = e-159  
Identities = 287/287 (100%)  
Strand = Plus / Plus

Query: 1257 atgctgggtccggtgaagggacaaccatgtacgccctctatatcaccgtccacgggtactt 1316  
|||||  
Sbjct: 5423 atgctgggtccggtgaagggacaaccatgtacgccctctatatcaccgtccacgggtactt 5482

Query: 1317 cctcatcaccttctctttggcatggtggtcctggccctggtggtctggaagatcttcac 1376  
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Sbjct: 5483 cctcatcaccttctctttggcatggtggtcctggccctggtggtctggaagatcttcac 5542

Query: 1377 cctgtcccgtgctacagcgggtcaaggagcgggggaagaaccggaagaaggtgctcacct 1436  
|||||  
Sbjct: 5543 cctgtcccgtgctacagcgggtcaaggagcgggggaagaaccggaagaaggtgctcacct 5602

Query: 1437 gctgggcctctcgagcctggtgggtgtgacatgggggttggccatcttcaccccggtggg 1496  
|||||  
Sbjct: 5603 gctgggcctctcgagcctggtgggtgtgacatgggggttggccatcttcaccccggtggg 5662

Query: 1497 cctctccaccgtctacatctttgcacttttcaactccttgcaaggtg 1543  
|||||  
Sbjct: 5663 cctctccaccgtctacatctttgcacttttcaactccttgcaaggtg 5709

Score = 563 bits (284), Expect = e-157  
Identities = 284/284 (100%)  
Strand = Plus / Plus

Query: 880 aggctttcccgaggagaggttcaagtcagaagatgccccaaagatccacgtggccctgggt 939  
|||||  
Sbjct: 3710 aggctttcccgaggagaggttcaagtcagaagatgccccaaagatccacgtggccctgggt 3769

Query: 940 ggcagcctgttcctcctgaatctggccttcttgggtcaatgtggggagtgggtcaaagggg 999  
|||||  
Sbjct: 3770 ggcagcctgttcctcctgaatctggccttcttgggtcaatgtggggagtgggtcaaagggg 3829

Query: 1000 tctgatgctgcctgctgggcccgggggctgtcttccactacttctgctctgtgccttc 1059  
|||||  
Sbjct: 3830 tctgatgctgcctgctgggcccgggggctgtcttccactacttctgctctgtgccttc 3889

Query: 1060 acctggatgggccttgaagccttccacctctacctgctcgctgtcagggctttcaacacc 1119  
|||||  
Sbjct: 3890 acctggatgggccttgaagccttccacctctacctgctcgctgtcagggctttcaacacc 3949

Query: 1120 tacttcgggcactacttctgaagctgagcctgggtgggctgggg 1163  
|||||  
Sbjct: 3950 tacttcgggcactacttctgaagctgagcctgggtgggctgggg 3993

Score = 228 bits (115), Expect = 9e-57  
Identities = 115/115 (100%)  
Strand = Plus / Plus

Query: 768 gagaccaccttggaccagtcacggtgcatatcctcacacgcatctcccaggcgggctg 827  
|||||  
Sbjct: 284 gagaccaccttggaccagtcacggtgcatatcctcacacgcatctcccaggcgggctg 343

Query: 828 tggggtctccatgatcttctggccttcaccattattctttatgcctttctgagg 882  
|||||  
Sbjct: 344 tggggtctccatgatcttctggccttcaccattattctttatgcctttctgagg 398

Score = 204 bits (103), Expect = 1e-49  
Identities = 103/103 (100%)  
Strand = Plus / Plus

Query: 1539 aggtgtcttcatctgctgctggttcaccatcctttacctccaagtcagagcaccacagt 1598  
|||||  
Sbjct: 8131 aggtgtcttcatctgctgctggttcaccatcctttacctccaagtcagagcaccacagt 8190

Query: 1599 ctctctcttactgcaagattggaccaggcccaactccgcatct 1641  
|||||  
Sbjct: 8191 ctctctcttactgcaagattggaccaggcccaactccgcatct 8233

Score = 204 bits (103), Expect = 1e-49  
Identities = 103/103 (100%)  
Strand = Plus / Plus

Query: 666 agggaccactggagactggtcttctgagggctgctccacggaggtcagacctgaggggac 725  
|||||  
Sbjct: 43 agggaccactggagactggtcttctgagggctgctccacggaggtcagacctgaggggac 102

Query: 726 cgtgtgctgctgtgaccacctgacctttttcgccctgctcctg 768  
|||||  
Sbjct: 103 cgtgtgctgctgtgaccacctgacctttttcgccctgctcctg 145

Score = 188 bits (95), Expect = 8e-45  
Identities = 95/95 (100%)  
Strand = Plus / Plus

Query: 1162 ggcctgcccgcctgatggcatcggcactgggagtgccaacagctacggcctctacacc 1221  
|||||  
Sbjct: 4169 ggcctgcccgcctgatggcatcggcactgggagtgccaacagctacggcctctacacc 4228

Query: 1222 atccgtgatagggagaaccgcacctctctggagct 1256  
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>AC018552.5.17437.94328  
Length = 76892

Score = 297 bits (150), Expect = 1e-77  
Identities = 150/150 (100%)  
Strand = Plus / Plus

Query: 57 aggtcaggaaaagcccaccgaagggccaagaaacacctgcctggggagcaacaacatgta 116  
|||||  
Sbjct: 68998 aggtcaggaaaagcccaccgaagggccaagaaacacctgcctggggagcaacaacatgta 69057

Query: 117 cgacatcttcaacttgaatgacaaggctttgtgcttcaccaagtgcaggcagtcgggcag 176  
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Sbjct: 69058 cgacatcttcaacttgaatgacaaggctttgtgcttcaccaagtgcaggcagtcgggcag 69117

Query: 177 cgactcctgcaatgtggaaaacttgcagag 206  
|||||  
Sbjct: 69118 cgactcctgcaatgtggaaaacttgcagag 69147

Score = 297 bits (150), Expect = 1e-77  
Identities = 150/150 (100%)  
Strand = Plus / Plus

Query: 344 aggttccgaggcaggtgatgaaggacgaggacaagccccctgacagagtgcgacttcca 403  
|||||  
Sbjct: 73847 aggttccgaggcaggtgatgaaggacgaggacaagccccctgacagagtgcgacttcca 73906

Query: 404 agagcctttttcgatccctgccaggcaacaggtctgtggtccgcttggccgtcaccattc 463  
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Sbjct: 73907 agagcctttttcgatccctgccaggcaacaggtctgtggtccgcttggccgtcaccattc 73966

Query: 464 tggacattggtccagggactctcttcaagg 493  
|||||  
Sbjct: 73967 tggacattggtccagggactctcttcaagg 73996

Score = 283 bits (143), Expect = 2e-73  
Identities = 143/143 (100%)  
Strand = Plus / Plus

Query: 205 agatactggctaaactacgaggcccatctgatgaaggaaggtttgacgcagaaggtgaac 264  
|||||  
Sbjct: 71877 agatactggctaaactacgaggcccatctgatgaaggaaggtttgacgcagaaggtgaac 71936

Query: 265 acgcctttcctgaaggctttggtccagaacctcagcaccaacactgcagaagacttctat 324  
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Sbjct: 71937 acgcctttcctgaaggctttggtccagaacctcagcaccaacactgcagaagacttctat 71996

Query: 325 ttctctctggagccctctcaggt 347  
|||||  
Sbjct: 71997 ttctctctggagccctctcaggt 72019

Score = 272 bits (137), Expect = 7e-70  
Identities = 141/142 (99%), Gaps = 1/142 (0%)  
Strand = Plus / Plus

Query: 487 ttca-aggggcccccggtcggcctgggagatggcagcggcggtgtgaacaatcgcttgt 545  
|||||  
Sbjct: 74849 ttcaaggggcccccggtcggcctgggagatggcagcggcggtgtgaacaatcgcttgt 74908

Query: 546 gggtttgagtgtgggacaaatgcatgtcaccaagctggctgagcctctggagatcgtctt 605  
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Sbjct: 74909 gggtttgagtgtgggacaaatgcatgtcaccaagctggctgagcctctggagatcgtctt 74968

Query: 606 ctctcaccagcgaccgccccct 627  
|||||  
Sbjct: 74969 ctctcaccagcgaccgccccct 74990

Score = 119 bits (60), Expect = 6e-24  
Identities = 60/60 (100%)  
Strand = Plus / Plus

Query: 1 atggcgacgcccaggggacctggggggccctgctcctgctcctcctgctcccgacctcaggt 60  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 64026 atggcgacgcccaggggacctggggggccctgctcctgctcctcctgctcccgacctcaggt 64085

Score = 81.8 bits (41), Expect = 1e-12  
Identities = 41/41 (100%)  
Strand = Plus / Plus

Query: 628 aacatgaccctcacctgtgtattctgggatgtgactaaagg 668  
||||||||||||||||||||||||||||||||||||  
Sbjct: 75495 aacatgaccctcacctgtgtattctgggatgtgactaaagg 75535



PubMed

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Protein

Genome

Structure

PMC

Taxonomy

OMIM

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Details

Display

default

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File

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Links

1: AC018552. Homo sapiens chro...[gi:27476108]

LOCUS AC018552 152156 bp DNA linear PRI 03-JAN-2003  
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 ACCESSION AC018552  
 VERSION AC018552.6 GI:27476108  
 KEYWORDS HTG.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 152156)  
 AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los  
 Alamos National Laboratory.  
 TITLE Direct Submission  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 152156)  
 AUTHORS DOE Joint Genome Institute.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-DEC-1999) Production Sequencing Facility, DOE Joint  
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 REFERENCE 3 (bases 1 to 152156)  
 AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los  
 Alamos National Laboratory.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-JAN-2003) DOE Joint Genome Institute, 2800 Mitchell  
 Drive, Walnut Creek, CA 94598, USA  
 COMMENT On Jan 3, 2003 this sequence version replaced gi:13786352.  
 Draft Sequence Produced by DOE Joint Genome Institute  
 www.jgi.doe.gov  
 Finishing Completed at Stanford Human Genome Center and Los Alamos  
 National Laboratory  
 www-shgc.stanford.edu  
 Quality: Phrap Quality >=40 99.8% of Sequence;  
 Estimated Total Number of Errors is 0.2.

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121 ctccccctgg cctacctgga gggctctgtc tgtcccttgg cctcactcc tcccaggga
181 agtgtctggc tgggcccac ctactgggc ctaggactg ctgcccttgg agtcaggggc
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